

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problems Mailbox.**

OM protein - protein search, using sw model  
Run on: September 3, 2003, 11:14:02 ; Search time 46.589 Seconds  
(without alignments)  
420.957 Million cell updates/sec

Title: US-08-325-278B-1\_COPY\_5\_80  
Perfect score: 389  
Sequence: 1 KEETPTPTDSEEVTKA.....GEYTDVADKGYTLNIKIFAG 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organellie:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

ALIGNMENTS

RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.

AC Q53291; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Protein LG (Fragment).

OS Streptococcus sp.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OC NCBI\_TaxID=1306;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93094283; PubMed=1460053;

RA Kihlberg B.M., Sjöbring U., Kasterl W., Björck L.;

RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";

RL J. Biol. Chem. 267:25583-25588(1992).

DR EMBL; S50809; AAA03280.1; -

DR HSP; P08654; IPGX.

DR InterPro; IPR003147; B1.

DR InterPro; IPR000724; IgG\_bind\_B.

DR Pfam; PF02246; B1; 4.

DR Pfam; PF01378; IgG-binding\_B; 2.

FT NON\_TER 455 455

SQ SEQUENCE 455 AA; 49926 MW; 381FC235B8C8307B CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	389	100.0 455 2 Q53291	Q53291 streptococ
2	389	100.0 719 2 Q51912	Q51912 peptostrept
3	298.5	76.7 992 2 Q51918	Q51918 peptostrept
4	85	21.9 1576 16 Q825V8	Q825V8 yerishnia pe
5	74	19.0 529 1 Q48937	Q48937 methanosarc
6	73.5	18.9 451 2 Q924J9	Q924J9 lactobacill
7	72	18.5 477 10 Q932G9	Q932G9 arabisdopsis
8	72	18.5 487 10 Q9STK2	Q9STK2 arabisdopsis
9	71.5	18.4 947 2 Q86487	Q86487 staphylococ
10	71	18.3 528 16 Q9KX8	Q9KX8 bacillus ha
11	71	18.3 929 3 P78718	P78718 nectria hae
12	70.5	18.1 955 16 Q8NXX7	Q8NXX7 staphylococ
13	70	18.0 645 5 Q33862	Q33862 ascaris suu
14	69.5	17.9 292 16 Q92FA8	Q92FA8 listeria in
15	69.5	17.9 300 11 Q9HY1	Q9HY1 rattus norv
16	69	17.7 190 17 Q8TQF1	Q8TQF1 methanosarc

Query Match 100.0%; Score 389; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. NO. 2.1e-30;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEETPTPTDSEEVTKANLIFANGSTOTAFKGTFFKATSEAYAYADTLKKNGEY 60  
Db 26 KEETPTPTDSEEVTKANLIFANGSTOTAFKGTFFKATSEAYAYADTLKKNGEY 85  
Qy 61 VDVAADKGYTLNIKIFAG 76  
Db 86 VDVAADKGYTLNIKIFAG 101

Q12191 saccharomyc  
Q9VMA7 drosophila  
Q8FHX3 escherichia  
Q9AJD4 streptococ  
Q9RI14 streptococ  
Q93U54 streptococ  
Q9PAQ0 xylella las  
Q8QK5 streptococ  
Q8TV18 methanopyru  
Q82T7 streptococ  
Q9S06 escherichia  
Q9AZB6 arabisdopsi  
Q01891 enterococu  
Q04111 enterococu  
Q45616 bacillus su  
Q8RK2 fusobacteri  
Q9X775 mycoplasma  
Q9J1C4 neisseria m  
Q47802 enterococu  
Q8KDD6 bacillus ha  
Q8THX7 methanosarc  
Q8X6R2 escherichia  
Q67097 aquifex aeo  
Q8K5Q0 streptococ  
Q9KKA4 rickettsia  
Q76641 caenorhabdi  
Q9CS77 mus musculu  
Q8PZM5 methanosarc

```

RESULT 2
Q51912
ID Q51912 PRELIMINARY; PRT; 719 AA.
AC Q51912;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerling U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1;
DR InterPro: IPR003147; BL.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 389; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KEETPTPTDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKKNGEY 60
|||||
98 KEETPTPTDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKKNGEY 157
|||||

Qy 61 VDVAADKGYTLNKFAG 76
Db 158 VDVAADKGYTLNKFAG 173
|||||

RESULT 3
Q51918
ID Q51918 PRELIMINARY; PRT; 992 AA.
AC Q51918;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjorck L., Sjoerling U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1;
DR InterPro: IPR003147; BL.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam; PF02246; B1; 5.
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 389; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KEETPTPTDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKKNGEY 60
|||||
98 KEETPTPTDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKKNGEY 157
|||||

Qy 61 VDVAADKGYTLNKFAG 76
Db 158 VDVAADKGYTLNKFAG 173
|||||

SEQUENCE FROM N.A.
STRAIN=312;
MEDLINE=95078460; PubMed=7987012;
Murphy J.P., Trueman A.R., Duggleby C.J.;
"Nucleotide sequence of the gene for peptostreptococcal protein L.";
DNA Seq. 4:259-265(1994).
-1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL; L04466; AAA67503.1;
HSP; O51911; IGAB.
InterPro: IPR003147; BL.
InterPro: IPR002988; GA.
InterPro: IPR001899; Gram_pos_anchor.
InterPro: IPR006192; LPXTG.
Pfam; PF02246; B1; 4.
Pfam; PF01468; GA; 4.
Pfam; PF00746; Gram_pos_anchor; 1.
TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
Cell wall; Peptidoglycan-anchor; Signal.
SIGNAL 1 24 POTENTIAL.
CHAIN 25 992 PROTEIN L.
SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 76.7%; Score 298.5; DB 2; Length 992;
Best Local Similarity 80.3%; Pred. No. 4.7e-21;
Matches 61; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

Qy 1 KEETPTPTDSEEVTKANLIFANGSTQTAFFKGTSEAYAYADTLKKNGEY 60
|||||
247 EKETPE-----PEEVTKANLIFADGSGTQNAEFGTFAKAYSAYADALKKNGEY 301
|||||

Qy 61 VDVAADKGYTLNKFAG 76
Db 302 VDVAADKGYTLNKFAG 317
|||||

RESULT 4
Q82EV8
ID Q82EV8 PRELIMINARY; PRT; 1576 AA.
AC Q82EV8;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative hemolysin.
GN YPO2045 OR Y2267.
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Versinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Versinia pestis KIM.";

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 ; Search time 44.137 Seconds  
(without alignments)  
420.957 Million cell updates/sec

Title: US-08-325-278b-1\_COPY\_81\_152

Perfect score: 371

Sequence: 1 KEKTPPEEKEVTIKANLIY.....GEYTVDDVADKGVTLNKIFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_plant:\*

10: sp\_rodent:\*

11: sp\_virus:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	371	100.0	455	2	Q53291	Q53291 streptococ
2	371	100.0	719	2	Q51912	Q51912 peptostrept
3	308	83.0	992	2	Q51918	Q51918 peptostrept
4	98.5	26.5	216	4	Q9BPV7	Q9BPV7 homo sapien
5	98.5	26.5	398	4	Q9BP21	Q9BP21 homo sapien
6	93.5	25.2	398	11	Q9C202	Q9C202 mus musculu
7	93.5	25.2	398	11	Q91WD1	Q91WD1 mus musculu
8	89.5	24.1	1576	16	Q8EVE8	Q8EVE8 versinia pe
9	73	19.7	588	2	Q9S0T6	Q9S0T6 escherichia
10	70	18.9	1498	5	Q9IDP2	Q9IDP2 plasmodium
11	69.5	18.7	256	5	Q27039	Q27039 theileria p
12	69.5	18.7	256	5	Q27029	Q27029 theileria p
13	69.5	18.7	279	2	Q9ADW8	Q9ADW8 ehrlichia c
14	69.5	18.7	280	5	Q27030	Q27030 theileria p
15	69.5	18.7	451	2	Q924J9	Q924J9 lactobacill
16	69.5	18.7	623	2	Q9F4L0	Q9F4L0 fibrobacter

17	69.5	18.7	623	2	Q9F109	Q9F109 fibrobacter
18	69	18.6	529	1	Q48937	Q48937 methanosarc
19	68.5	18.5	243	17	Q9YFE6	Q9YFE6 acropyrum p
20	68.5	18.5	280	4	Q92637	Q92637 homo sapien
21	68.5	18.5	374	4	Q92663	Q92663 homo sapien
22	68.5	18.5	375	4	Q92495	Q92495 homo sapien
23	67	18.1	492	17	Q973M8	Q973M8 sulfolobus
24	67	18.1	1433	2	Q45616	Q45616 bacillus su
25	66.5	17.9	171	6	Q95N20	Q95N20 sus scrofa
26	66.5	17.9	227	6	Q95N21	Q95N21 sus scrofa
27	66.5	17.9	256	6	Q95N22	Q95N22 sus scrofa
28	66.5	17.9	333	3	Q9UVE8	Q9UVE8 yarrowia li
29	66.5	17.9	357	6	Q8SPW5	Q8SPW5 macaca fasc
30	66	17.8	448	10	Q9SKP0	Q9SKP0 arabidopsis
31	66	17.8	585	16	Q8EJS9	Q8EJS9 shewanella
32	66	17.8	873	2	Q926H6	Q926H6 lactococcus
33	65.5	17.7	108	2	P72105	P72105 neisseria m
34	65.5	17.7	496	16	Q8F022	Q8F022 leptospira
35	65.5	17.7	718	16	Q98RK2	Q98RK2 mycoplasma
36	65.5	17.7	1167	17	Q8TUJ9	Q8TUJ9 methanosarc
37	65.5	17.7	4545	2	Q9X4W2	Q9X4W2 vibrio chol
38	65.5	17.7	4558	16	Q9KS12	Q9KS12 vibrio chol
39	65	17.5	359	5	Q9VBT9	Q9VBT9 drosophila
40	65	17.5	377	16	Q8CT26	Q8CT26 staphylococ
41	65	17.5	420	5	Q8T4C5	Q8T4C5 drosophila
42	65	17.5	420	5	Q8T3P4	Q8T3P4 drosophila
43	65	17.5	425	16	Q9K491	Q9K491 streptomyce
44	64.5	17.4	188	10	Q9LEH5	Q9LEH5 hordeum vul
45	64.5	17.4	383	5	Q9VTV4	Q9VTV4 drosophila

## ALIGNMENTS

## RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.  
AC Q53291;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Protein LG (Fragment).  
OS Streptococcus sp.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93094283; PubMed=1460053;  
RA Kihlberg B.M., Sjöbring U., Kaster W., Björck L.;  
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties.";  
RL J. Biol. Chem. 267:25583-25588(1992).  
DR EMBL; S50809; AAA03280.1; .  
DR HSSP; P06654; IPOX.  
DR InterPro; IPR003147; BI.  
DR InterPro; IPR000724; Igc\_bind\_B.  
DR Pfam; PF02246; BI; 4.  
DR Pfam; PF01378; Igc\_binding\_B; 2.  
FT NON\_TER 455 455  
SQ SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;

Query Match 100.0%; Score 371; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.7e-29;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTPPEEKEVTIKANLIYADGKTQTAEFGTGTETAEAYRYADALKKNGEYTVDDA 60  
|||||  
DB 102 KEKTPPEEKEVTIKANLIYADGKTQTAEFGTGTETAEAYRYADALKKNGEYTVDDA 161  
QY 61 DKGYTLNKFAG 72  
|||||  
DB 162 DKGYTLNKFAG 173

```
RESULT 2
Q51912
ID Q51912 PRELIMINARY; PRT: 719 AA.
AC Q51912;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjoerck L., Sjoerding U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 719
FT CHAIN 19 719 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 60
DB 174 KEKTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 233
QY 61 DKGYTLNKKFAG 72
DB 234 DKGYTLNKKFAG 245

RESULT 3
Q51918
ID Q51918 PRELIMINARY; PRT: 992 AA.
AC Q51918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein L precursor.
OS Peptostreptococcus magnus.
OC Bacteria; Firmicutes; Clostridia; Clostridiales;
OC Peptostreptococcaceae; Finegoldia.
OX NCBI_TaxID=1260;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=90215984; PubMed=2108927;
RA Kastern W., Holst E., Nielsen E., Sjoerding U., Bjorck L.;
RT "Protein L, a bacterial immunoglobulin-binding protein and possible
virulence determinant.";
RL Infect. Immun. 58:1217-1222(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=312;
RX MEDLINE=92316971; PubMed=1618782;
RA Bjoerck L., Sjoerding U., Kastern W.;
RT "Structure of peptostreptococcal protein L and identification of
repeated immunoglobulin light chain-binding domain.";
RL J. Biol. Chem. 267:12820-12825(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; M86697; AAA25612.1; -.
DR InterPro: IPR003147; B1.
DR InterPro: IPR004829; Csurface_antigen.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 5.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 719
FT CHAIN 19 719 POTENTIAL.
FT CHAIN 19 719 PROTEIN L.
SQ SEQUENCE 719 AA; 78983 MW; 963A8D76D5E34DD2 CRC64;

Query Match 100.0%; Score 371; DB 2; Length 719;
Best Local Similarity 100.0%; Pred. No. 8.1e-29;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEKTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 60
DB 174 KEKTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVA 233
QY 61 DKGYTLNKKFAG 72
DB 234 DKGYTLNKKFAG 245
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=3316;
RX MEDLINE=95078460; PubMed=7987012;
RA Murphy J.P., Trowern A.R., Duggleby C.J.;
RT "Nucleotide sequence of the gene for peptostreptococcal protein L.";
RL DNA Seq. 4:259-265(1994).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1; -.
DR HSSP: Q51911; 1GAB.
DR InterPro: IPR003147; B1.
DR InterPro: IPR002988; GA.
DR InterPro: IPR001899; Gram_pos_anchor.
DR InterPro: IPR006192; LPXTG.
DR Pfam: PF02246; B1; 4.
DR Pfam: PF01468; GA; 4.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR TIGRFAMs: TIGR01167; LPXTG_anchor; 1.
DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 992
FT CHAIN 25 992 POTENTIAL.
FT CHAIN 25 992 PROTEIN L.
SQ SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 83.0%; Score 308; DB 2; Length 992;
Best Local Similarity 84.3%; Pred. No. 2.5e-22;
Matches 59; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 3 KTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 62
DB 468 ETEPEKKEVIKYNLIADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 527
QY 63 GYTINIKFAG 72
DB 528 GYTINIKFAG 537

RESULT 4
Q9BPV7
ID Q9BPV7 PRELIMINARY; PRT: 216 AA.
AC Q9BPV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to BNS1 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEF-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003039; AAH03039.1; -.
DR EMBL; BC00516; AAH00516.1; -.
SQ SEQUENCE 216 AA; 24806 MW; F29028AEACA8DB04 CRC64;

Query Match 26.5%; Score 98.5; DB 4; Length 216;
Best Local Similarity 34.6%; Pred. No. 0.04;
Matches 28; Conservative 10; Mismatches 24; Indels 19; Gaps 3;

QY 3 KTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 50
DB 66 KTEPEKKEVTIKANLIYADGKTQTAEFGTAEATAYADALKKDNGETYVDVADK 120
QY 51 DNGETYVDVADK--YTLNKK 69
DB 121 GNWTKTVDSMDGMPSHIINIK 141

RESULT 5
Q9BP21
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 : Search time 44.137 Seconds  
(without alignments)  
420.957 Million cell updates/sec

Title: US-08-325-278b-1\_COPY\_153\_224

Perfect score: 369  
Sequence: 1 KETTPPEPKKEVTIKANLIY.....GKTYVDVADKGYTLNIRKAG 72

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*\*

- 1: sp\_archaea:\*\*
- 2: sp\_bacteria:\*\*
- 3: sp\_fungi:\*\*
- 4: sp\_human:\*\*
- 5: sp\_invertebrate:\*\*
- 6: sp\_mammal:\*\*
- 7: sp\_mhc:\*\*
- 8: sp\_organelle:\*\*
- 9: sp\_phage:\*\*
- 10: sp\_plant:\*\*
- 11: sp\_rodent:\*\*
- 12: sp\_virus:\*\*
- 13: sp\_vertebrate:\*\*
- 14: sp\_unclassified:\*\*
- 15: sp\_virus:\*\*
- 16: sp\_bacteriaph:\*\*
- 17: sp\_archaeap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	455	Q53291	streptococc
2	369	100.0	719	Q51912	peptostrept
3	315	85.4	992	Q51918	peptostrept
4	88.5	24.0	216	Q9BPV7	Q9BPV7 homo sapien
5	88.5	24.0	398	Q9BPZ1	Q9BPZ1 homo sapien
6	83.5	22.6	398	Q9CZ02	Q9CZ02 mus musculu
7	83.5	22.6	398	Q91WD1	Q91WD1 mus musculu
8	82.5	22.4	1576	Q8ZEV8	Q8ZEV8 arsinia pe
9	74	20.1	871	Q9LME2	Q9LME2 arabinidopsi
10	73.5	19.9	256	Q27039	Q27039 thelleria p
11	73.5	19.9	256	Q27029	Q27029 thelleria p
12	73.5	19.9	280	Q27030	Q27030 thelleria p
13	72	19.5	1025	Q9LME3	Q9LME3 arabinidopsi
14	71	19.2	265	Q23822	Q23822 dunaliella
15	69	18.7	324	Q9UUK3	Q9UUK3 schizosacch
16	68	18.4	448	Q9SKP0	Q9SKP0 arabinidopsi

17	67.5	18.3	383	5	O9VTV4
18	67	18.2	946	2	O9EV24
19	67	18.2	953	2	O9ETX2
20	67	18.2	953	2	O9EV29
21	67	18.2	953	2	O9EV25
22	67	18.2	953	2	O9ETG5
23	67	18.2	953	2	O9EV23
24	67	18.2	953	2	O9EV34
25	67	18.2	1204	2	O8GM76
26	66.5	18.0	657	16	O92DS2
27	66	17.9	418	10	O96246
28	66	17.9	477	16	O8UDR8
29	66	17.9	1096	2	O8GM79
30	66	17.9	1098	2	O48152
31	66	17.9	1498	5	O8IDP2
32	65.5	17.8	436	5	O21481
33	65.5	17.8	451	2	O9Z4J9
34	65.5	17.8	476	16	O8FBV2
35	65.5	17.8	1167	17	O8TUJ9
36	65.5	17.8	1210	2	O8GM75
37	65.5	17.8	1210	2	O8GM74
38	65.5	17.8	4545	2	O9X4W2
39	65.5	17.8	4558	16	O9KS12
40	65	17.6	284	5	O76174
41	65	17.6	284	5	O9TYA5
42	65	17.6	636	16	O51624
43	65	17.6	838	16	O84625
44	64.5	17.5	243	17	O9VFE6
45	64.5	17.5	333	3	O9UVE8

#### ALIGNMENTS

#### RESULT 1

Q53291 ID Q53291 PRELIMINARY; PRT; 455 AA.  
AC Q53291;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Protein LG (fragment)  
OS Streptococcus sp.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93094283; PubMed=1460053;  
RA Kihlberg B.M., Sjöbring U., Kastern W., Björck L.;  
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";  
RL J. Biol. Chem. 267:25583-25588(1992).  
DR EMBL; S50809; AAA03280.1; -;  
DR HSSP; P06654; IpgX.  
DR InterPro; IPR003147; B1.  
DR InterPro; IPR000724; Igg\_bind\_B.  
DR Pfam; PF02246; B1; 4.  
DR Pfam; PF01378; Igg\_binding\_B; 2.  
FT NON\_TER 455 455  
SQ SEQUENCE 455 AA: 49926 MW: 381FC235BBC8307B CRC64:

Query Match 100.0%; Score 369; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 2.4e-29;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy	1	KETTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEETAEAYRYADLLAKENGYTVDA 60
Db	174	KETTPPEPKKEVTIKANLIYADGKTQTAEFGKTFEETAEAYRYADLLAKENGYTVDA 233
Qy	61	DGYTLNIRKAG 72
Db	234	DGYTLNIRKAG 245

O9vtv4	drosophila
O9ev24	mannheimia
O9etx2	mannheimia
O9ev29	pasteurella
O9ev25	mannheimia
O9etg5	pasteurella
O9ev23	mannheimia
O9ev34	pasteurella
O8gm76	haemophilus
O92ds2	listeria in
O96246	arabidopsis
O8udr8	agrobacteri
O8gm79	haemophilus
O48152	haemophilus
O8idp2	plasmodium
O21481	caenorhabdi
O9z4j9	lactobacilli
O8fbv2	escherichia
O8tu9	methanosarc
O8gm75	haemophilus
O8gm74	haemophilus
O9x4w2	vibrio chol
O9ks12	vibrio chol
O76174	thelateria s
O9tya5	thelateria s
O51624	borrelia bu
O84625	chlamydia t
O9vfe6	aeropyrum p
O9uve8	yarrowia li

```

RP SEQUENCE FROM N.A.
RC STRAIN-3316;
RX MEDLINE-95078460; PubMed-7987012;
RT Murphy J.P., Towern A.R., Duggleby C.J.;
RA Nucleotide sequence of the gene for peptostreptococcal protein L.*;
RL DNA Seq. 4:259-265(1994)
CC 1- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
CC AN AMIDE BOND (BY SIMILARITY).
DR EMBL; L04466; AAA67503.1; -
DR HSSP; Q51911; IGAB.
DR InterPro; IPR003147; B1.
DR InterPro; IPR002988; GA.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF02246; B1; 4.
DR Pfam; PF01468; GA; 4.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25; 992 PROTEIN L.
FT CHAIN 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;
SQ SEQUENCE 992 AA; 108700 MW; 9CFF5771578A5DCE CRC64;

Query Match 85.4%; Score 315; DB 2; Length 992;
Best Local Similarity 85.7%; Pred. No. 1.9e-23;
Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0

QY 3 KTEEPKEEVTIKANLIYADGKTQTAEPKGFTEETAAYRYADLLAKENGYTVDVADK 62
Db 468 ETPEEPKEEVTIKVNLFIADGKTQTAEPKGFTEETAAYRYADLLAKVNGYTDLEDG 527
QY 63 GYTLNIKFAG 72
Db 528 GYTLNIKFAG 537

RESULT 4
Q9BPV7 PRELIMINARY; PRT; 216 AA.
ID Q9BPV7
AC AC
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to BN31 (BHK21) temperature sensitivity complementing.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003039; AAH03039.1; -
DR EMBL; BC000516; AAH00516.1; -
SQ SEQUENCE 216 AA; 24806 MW; F29028AEACA8D804 CRC64;

Query Match 24.0%; Score 88.5; DB 4; Length 216;
Best Local Similarity 33.3%; Pred. No. 0.33;
Matches 27; Conservative 9; Mismatches 26; Indels 19; Gaps 3;

QY 3 KTEEPKEEVTIKANLIYAD-----GKTOTAETKGTFFETAAYRYADLLAK 50
Db 66 KIKEEPKEEVTIVKKEKREDRDRQEGHGRGRPEVIQSHSIFEGGPAEMMK-----KK 120
QY 51 ENGYTVDVADKG--YTLNIK 69
Db 121 GNWQKTVDSVDMGSPSHIINIK 141

RESULT 5
Q9BP21

```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds  
(without alignments)  
406.975 Million cell updates/sec

Title: US-08-325-278B-1\_COPY\_153\_224

Perfect score: 369

Sequence: 1 KETTPPEPKEVTIKANLIY.....GKTYVDVADKGYTLNIKFPAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	455	2 A45063	immunoglobulin-bin
2	369	100.0	719	2 A42808	Ig light chain-bin
3	315	85.4	992	2 S54396	protein L precursor
4	162	43.9	74	2 A34483	Ig light chain-bin
5	82.5	22.4	1576	2 AB0249	probable hemolysin
6	80.5	21.8	395	2 A43700	BN51 protein - hum
7	74	20.1	871	2 D86355	protein T16B15.12
8	73.5	19.9	256	2 S54803	merozoite surface
9	72	19.5	1025	2 E86355	hypothetical prote
10	69	18.7	324	2 T37931	hypothetical coile
11	68	18.4	448	2 H84782	late embryogenesis
12	67	18.2	953	1 B30169	leukotoxin A - Pas
13	66.5	18.0	657	2 AD1525	probable cell surf
14	66	17.9	448	2 JC6171	late embryogenesis
15	66	17.9	470	2 A28288	RNA dependent oxid
16	66	17.9	477	2 D97606	glycolate oxidase
17	65.5	17.8	436	2 T16638	hypothetical prote
18	65.5	17.8	476	1 W2EC	tryptophanase (sc
19	65.5	17.8	476	2 E91209	tryptophanase (imp
20	65.5	17.8	476	2 H86055	tryptophanase (imp
21	65.5	17.8	1179	2 T35033	DNA-directed DNA p
22	65.5	17.8	4558	2 C82139	RTX toxin REXA VCI
23	65	17.6	636	2 H70184	methyl-accepting c
24	65	17.6	838	2 D71492	hypothetical prote
25	64.5	17.5	243	2 F72719	hypothetical prote
26	64	17.3	621	2 S49020	nuclear lamin C pr
27	64	17.3	722	2 T21521	hypothetical prote
28	63.5	17.2	414	2 S48738	potassium channel
29	63.5	17.2	425	2 S52852	inward rectifier p

30 63.5 17.2 479 2 T47561 late embryogenesis  
31 63 17.1 88 2 C83657 hypothetical prote  
32 63 17.1 319 2 H98872 hypothetical prote  
33 63 17.1 693 2 H95255 choline binding pr  
34 63 17.1 6642 2 T29757 protein UNC-89 - C  
35 62.5 16.9 423 2 I38979 inward rectifier p  
36 62.5 16.9 425 2 I48202 potassium channel-  
37 62 16.8 118 2 S38717 Ig heavy chain V r  
38 62 16.8 195 2 A70247 conserved hypothet  
39 62 16.8 356 2 T37136 hypothetical prote  
40 62 16.8 529 2 S62194 hypothetical prote  
41 62 16.8 1612 2 AB1347 probable peptidogl  
42 61.5 16.7 266 2 A12289 hypothetical prote  
43 61.5 16.7 280 2 S35103 bone sialoprotein  
44 61.5 16.7 451 1 D64424 tldd homolog MU099  
45 61.5 16.7 487 2 T10215 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

A45063 immunoglobulin-binding protein LG - Peptostreptococcus magnus

C/Species: Peptostreptococcus magnus

C/Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Oct-1999

C/Accession: A45063

R/Kihlberg, B.M.; Sjoerding, U.; Kastern, W.; Bjoerck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A/Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties

A/Reference number: A45063; MUID:93094283; PMID:1460053

A/Accession: A45063

A/Status: preliminary

A/Molecule type: mRNA; protein

A/Residues: 1-455 <KH>

A/Cross-references: GB:S50809; NID:G261705; PIDN:AAA03280.1; PID:G261706

A/Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBI:P:120303)

Query Match 100.0%; Score 369; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 6.8e-31;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETTPPEPKEVTIKANLIYADGKTQTAEFKCTFEATAEAYRYADLLAKENGYTVDVA 60  
DB 174 KETTPPEPKEVTIKANLIYADGKTQTAEFKCTFEATAEAYRYADLLAKENGYTVDVA 233

QY 61 DKGYTLNIKFPAG 72

DB 234 DKGYTLNIKFPAG 245

##### RESULT 2

A42808 Ig light chain-binding protein precursor - Peptostreptococcus magnus

N/Alternate names: protein L

C/Species: Peptostreptococcus magnus

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C/Accession: A42808; A41493

R/Kastern, W.; Sjoerding, U.; Bjoerck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A/Title: Structure of peptostreptococcal protein L and identification of a repeated

A/Reference number: A42808; MUID:92316971; PMID:1618782

A/Accession: A42808

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-719 <KAS>

A/Cross-references: GB:M86697

R/Kastern, W.; Holst, B.; Nielsen, E.; Sjoerding, U.; Bjoerck, L.

Infect. Immun. 58, 1217-1222, 1990

A/Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulenc

A/Reference number: A41493; MUID:90215984; PMID:2108927

A/Accession: A41493

A/Status: preliminary



```

A:Molecule type: DNA
A:Residues: 202-275 <KA2>
C:Keywords: immunoglobulin

      Query Match      100.0%;      Score 369;      DB 2;      Length 719;
      Best Local Similarity 100.0%;      Pred. NO. 1.1e-30;
      Matches 72;      Conservative 0;      Mismatches 0;      Indels 0;      Gaps 0;

QY      1      KETPTPEPEEVIKANIIVADGKTQTAEKPGTFEEATAEAYRYADLLAKENGKYYTDVA 60
      |||||
Db      246      KETPTPEPEEVIKANIIVADGKTQTAEKPGTFEEATAEAYRYADLLAKENGKYYTDVA 305
      |||||

QY      61      DKGYTLNLIKFPAG 72
      |||||
Db      306      DKGYTLNLIKFPAG 317
      |||||

```

RESULT 3  
396  
L precursor - Peptostreptococcus magnus (strain 3316)  
Species: Peptostreptococcus magnus  
A/Variety: strain 3316  
C/Date: 27-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 15-Oct-1999  
C/Accession: S54396  
R/Murphy, J.P.; Duggieby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.F.F.  
Mol. Microbiol. 12, 911-920, 1994  
A/Title: The functional units of a peptostreptococcal protein L.  
A/Reference number: S54396; MUID:95020613; PMID:7934898  
A/Accession: S54396  
A/Status: preliminary; nucleic acid sequence not shown

```

A:Molecule type: DNA
A:Residues: 1-992 <MUR>
A:Cross-references: EMBL:L04466; NID:G150673; PIDN:AAA67503.1; PID:G150674

      Query Match      85.4%; Score 315; DB 2; Length 992;
      Best Local Similarity 85.7%; Pred. No. 7.1e-25;
      Matches 60; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      3 KTPREPKEVITKANLIYADGKTQTAAEPKGFEEATAEAYRYADLLAKENGKITYTVDVADK 62
      |||||
Db      468 ETPEEPKEVITKVNLIIPADGKTQTAAEPKGFEEATAEAYRYADLLAKVNGEYTDLEDG 527
      |||||

QY      63 GYTLNIKFPAG 72
      |||||
Db      528 GYTLNIKFPAG 537
      |||||

```

C:Species: *Reptostreptococcus magnus*  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Aug-1996  
 C:Accession: A34483  
 R:Akerstrom, B.; Bjoerck, L.  
 J. Biol. Chem. 264, 19740-19746, 1989  
 A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteri  
 A:Reference number: A34483; PMID:9062074; PMID:2479638  
 A:Accession: A34483  
 A:Molecule type: protein  
 A:Residues: 1-74 <AKE>  
 C:Keywords: immunoglobulin

```

Query Match      43.9%; Score 162; DB 2; Length 74;
Best Local Similarity 62.5%; Pred. No. 4e-10;
Matches 35; Conservative 3; Mismatches 2; Indels 16; Gaps 1;

QY 2 EKTPEEPKGEVITKANLIYADGKGTQTAEPKG-----TPEETAEEA 41
| | | | | | | | | | | | | | | | : | | | |
DB 9 ETTPEEPKGEVITKANLIYADGKGTAEFKGPEETPEKPFEVDGVASIEEATAAA 64
| | | | | | | | | | | | | | | | : | | | |

RESULT 5
~0249
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:02 : Search time 44.137 Seconds  
(without alignments)  
420.937 Million cell updates/sec

Title: US-08-325-278b-1\_COPY\_225\_296  
Perfect score: 370  
Sequence: 1 KEKTEPEEKEVITKANLIY.....GKYTADLEDGGYTINIRFAG 72

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_23:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phage:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	100.0	455	2 Q53291	Q53291 streptococc
2	370	100.0	719	2 Q51912	Q51912 peptostrept
3	329	88.9	992	2 Q51918	Q51918 peptostrept
4	80.5	21.8	1576	16 Q8ZEY8	Q8ZEY8 versinia pe
5	74	20.0	324	3 Q90UK3	Q90UK3 schizosacch
6	74	20.0	846	2 Q8RPV1	Q8RPV1 streptococc
7	71.5	19.3	216	4 Q9BPV7	Q9BPV7 homo sapien
8	71.5	19.3	398	4 Q9BP21	Q9BP21 homo sapien
9	71.5	19.3	657	16 Q92DS2	Q92DS2 listeriopsis
10	71	19.2	871	10 Q9LME2	Q9LME2 arabidopsis
11	70.5	19.1	256	5 Q27039	Q27039 theileria p
12	70.5	19.1	256	5 Q27029	Q27029 theileria p
13	70.5	19.1	280	5 Q27030	Q27030 theileria p
14	70.5	19.1	398	11 Q9CZ02	Q9CZ02 mus musculu
15	70.5	19.1	398	11 Q9LWD1	Q9LWD1 mus musculu
16	70	18.9	549	17 Q8TZL6	Q8TZL6 pyrococcus

17	69.5	18.8	1086	10 Q9SGU0	Q9SGU0 arabidopsis
18	69.5	18.8	1849	2 Q9SAK2	Q9SAK2 lactobacilli
19	69.5	18.8	2062	10 Q9CJ32	Q9CJ32 arabidopsis
20	69	18.6	397	16 Q92ED7	Q92ED7 listeria in
21	69	18.6	401	16 Q92ED5	Q92ED5 listeria in
22	69	18.6	1025	10 Q9LME3	Q9LME3 arabidopsis
23	68.5	18.5	858	10 Q9SGT8	Q9SGT8 arabidopsis
24	67.5	18.2	383	5 Q9VTVA	Q9VTVA drosophila
25	67	18.1	278	10 Q94KL8	Q94KL8 podophyllum
26	67	18.1	283	3 Q93337	Q93337 saccharomyc
27	66.5	18.0	1029	10 Q9SGT9	Q9SGT9 arabidopsis
28	66	17.8	495	16 Q9WGB8	Q9WGB8 staphylococ
29	65.5	17.7	225	2 Q9WX49	Q9WX49 onion yello
30	65.5	17.7	4545	2 Q9X4W2	Q9X4W2 vibrio chol
31	65.5	17.7	4558	16 Q9KSI2	Q9KSI2 vibrio chol
32	65	17.6	304	6 Q9BE26	Q9BE26 macaca fasc
33	65	17.6	319	4 Q00477	Q00477 homo sapien
34	65	17.6	334	4 Q9NR44	Q9NR44 homo sapien
35	65	17.6	334	4 Q9BU81	Q9BU81 homo sapien
36	65	17.6	357	4 Q15338	Q15338 homo sapien
37	65	17.6	359	4 P78410	P78410 homo sapien
38	65	17.6	495	4 Q9HCY1	Q9HCY1 homo sapien
39	65	17.6	513	4 Q00481	Q00481 homo sapien
40	65	17.6	584	4 Q00478	Q00478 homo sapien
41	64.5	17.4	279	2 Q9ADV8	Q9ADV8 ehrlichia c
42	64	17.3	500	16 Q8NY41	Q8NY41 staphylococ
43	64	17.3	585	16 Q8EJS9	Q8EJS9 shewanella
44	64	17.3	1433	2 Q45616	Q45616 bacillus su
45	63.5	17.2	183	16 Q8EBW9	Q8EBW9 shewanella

ALIGNMENTS

RESULT 1

Q53291 Q53291 PRELIMINARY; PRT; 455 AA.  
ID AC Q53291  
AD Q53291:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Protein LG (Fragment).  
OS Streptococcus sp.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae.  
OC Streptococcus.  
OC NCBI\_TaxID=1306;  
OX [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=93094283; PubMed=1460053;  
RX Kihlberg B.M., Sjobring U., Kastern W., Rjorck L.:  
RT "Protein LG: a hybrid molecule with unique immunoglobulin binding properties";  
RL J. Biol. Chem. 267:25583-25588(1992).  
DR EMBL; S50809; AAA03280.1; -;  
DR HSSP; P06654; IPGX.  
DR InterPro; IPR003147; BI.  
DR InterPro; IPR000724; Igg\_bind\_B.  
DR Pfam; PF02246; BI; 4.  
DR Pfam; PF01378; Igg\_binding\_B; 2.  
FT NON\_TER 455 455  
SQ SEQUENCE 455 AA; 49926 MW; 381FC235BBC8307B CRC64;

Query Match 100.0%; Score 370; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 6.5e-30;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KEKTEPEEKEVITKANLIYADGKTKTQTAETFAETAEAYRYADLLAKENGKYTABLE 60
Db	246	KEKTEPEEKEVITKANLIYADGKTKTQTAETFAETAEAYRYADLLAKENGKYTABLE 305
QY	61	DGGYTINIRFAG 72
Db	306	DGGYTINIRFAG 317



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2003, 11:14:37 ; Search time 17.0137 Seconds  
(without alignments)  
406.975 Million cell updates/sec

Title: US-08-325-278b-1\_COPY\_225\_296

Perfect score: 370

Sequence: 1 KEKTPPEPKKEVTIKANLIY.....CKYTADLEDGGYTINIRFAG 72

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	100.0	455	2 A45063	immunoglobulin-bin
2	370	100.0	719	2 A42808	Ig light chain-bin
3	329	88.9	992	2 S54356	protein L precursor
4	157	42.4	74	2 A34483	Ig light chain-bin
5	80.5	21.8	1576	2 AE0249	probable hemolysin
6	74	20.0	324	2 T37931	hypothetical coile
7	71.5	19.3	657	2 AD1525	probable cell surf
8	71	19.2	871	2 D86355	protein Tl6E15.12
9	70.5	19.1	256	2 S54803	merozoite surface
10	69.5	18.8	2062	2 G96602	probable receptor
11	69	18.6	397	2 AC1498	specificity determ
12	69	18.6	401	2 AE1498	specificity determ
13	69	18.6	1025	2 E86355	hypothetical prote
14	68.5	18.5	858	2 E96602	hypothetical prote
15	67	18.1	283	2 S69639	hypothetical prote
16	66.5	18.0	1039	2 E96602	hypothetical prote
17	66	17.8	495	2 D89808	hypothetical prote
18	65.5	17.7	4558	2 C82199	hypothetical prote
19	64.5	17.4	1179	2 T35093	RTX toxin REXA VC1
20	64	17.3	863	2 S06017	DNA-directed DNA p
21	64	17.3	2364	2 A56577	neuraxin - rat
22	64	17.3	2464	1 QRMSP1	microtubule-associ
23	63.5	17.2	395	2 A43700	microtubule-associ
24	63.5	17.2	550	2 F75186	BN51 protein - hum
25	63	17.0	356	2 T37136	thermosome, chain
26	63	17.0	490	2 F38462	hypothetical prote
27	63	17.0	1104	1 A36866	S-mephenytoin 4'-h
28	62.5	16.9	215	2 AC1156	microbial collagen
29	62	16.8	286	2 A12289	transcription regu
					hypothetical prote

ALIGNMENTS

RESULT 1

A45063

immunoglobulin-binding protein LG - Peptostreptococcus magnus

C:Species: Peptostreptococcus magnus

C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Oct-1999

C:Accession: A45063

R:Kihlberg, B.M.; Sjobring, U.; Kastern, W.; Bjoerck, L.

J. Biol. Chem. 267, 25583-25588, 1992

A:Title: Protein LG: a hybrid molecule with unique immunoglobulin binding properties

A:Reference number: A45063; MUID:93094283; PMID:1460053

A:Accession: A45063

A:Status: preliminary

A:Molecule type: mRNA; protein

A:Residues: 1-455 <KIH>

A:Cross-references: GB:S50809; NID:g261705; PIDN:AAA03280.1; PID:g261706

A:Note: sequence extracted from NCBI backbone (NCBIN:120302, NCBIP:120303)

Query Match: 100.0%; Score 370; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-32;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KEKTPPEPKKEVTIKANLIYADGKTQTAEPKGFATATAYRYADLLAKENGYTADLE 60

Db 246 KEKTPPEPKKEVTIKANLIYADGKTQTAEPKGFATATAYRYADLLAKENGYTADLE 305

Qy 61 DGGYTINIRFAG 72

Db 306 DGGYTINIRFAG 317

RESULT 2

A42808

Ig light chain-binding protein precursor - Peptostreptococcus magnus

N:Alternate names: protein L

C:Species: Peptostreptococcus magnus

C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C:Accession: A42808; A41493

R:Kastern, W.; Sjoebbring, U.; Bjoerck, L.

J. Biol. Chem. 267, 12820-12825, 1992

A:Title: Structure of peptostreptococcal protein L and identification of a repeated

A:Reference number: A42808; MUID:92316971; PMID:1618782

A:Accession: A42808

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <KAS>

A:Cross-references: GB:M86697

R:Kastern, W.; Holst, E.; Nielsen, E.; Sjoebbring, U.; Bjoerck, L.

Infect. Immun. 59, 1217-1222, 1990

A:Title: Protein L, a bacterial immunoglobulin-binding protein and possible virulence

A:Reference number: A41493; MUID:90215984; PMID:2108927

A:Accession: A41493

A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 202-275 <KA2>  
C:Keywords: immunoglobulin

Query Match 100.0%; Score 370; DB 2; Length 719;  
Best Local Similarity 100.0%; Pred. No. 7.2e-32;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KETPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGYTADLE 60  
|||||  
Db 318 KETPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGYTADLE 377  
|||||  
QY 61 DGGYTINIRFAG 72  
|||||  
Db 378 DGGYTINIRFAG 389  
|||||

## RESULT 3

S54396  
Protein L precursor - Peptostreptococcus magnus (strain 3316)  
C:Species: Peptostreptococcus magnus  
C:Accession: S54396  
C:Date: 27-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 15-Oct-1999  
R:Murphy, J.P.; Duggleby, C.J.; Atkinson, M.A.; Trowern, A.R.; Atkinson, T.; Goward, C.F.  
Mol. Microbiol. 12, 911-920, 1994  
A:Title: The functional units of a peptostreptococcal protein L.  
A:Reference number: S54396; MUID:95020613; PMID:7934898  
A:Accession: S54396  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-992 <MUR>  
A:Cross-references: EMBL:L04466; NID:g150573; PIDN:AAA67503.1; PID:g150674

Query Match 88.9%; Score 329; DB 2; Length 992;  
Best Local Similarity 90.0%; Pred. No. 2.7e-27;  
Matches 63; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 3 KTPPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGYTADLE 62  
|||||  
Db 468 ETPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGYTADLE 527  
|||||  
QY 63 GYTINIRFAG 72  
|||||  
Db 528 GYTINIRFAG 537  
|||||

## RESULT 4

S54483  
light chain-binding protein L - Peptostreptococcus magnus (fragments)  
C:Species: Peptostreptococcus magnus  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Aug-1996  
C:Accession: A34483  
R:Akerstroem, B.; Bjoerck, L.  
J. Biol. Chem. 264, 19740-19746, 1989  
A:Title: Protein L: an immunoglobulin light chain-binding bacterial protein. Characteriz  
A:Reference number: A34483; MUID:90062074; PMID:2479638  
A:Accession: A34483  
A:Molecule type: protein  
A:Residues: 1-74 <AKE>  
C:Keywords: immunoglobulin

Query Match 42.4%; Score 157; DB 2; Length 74;  
Best Local Similarity 62.7%; Pred. No. 4.8e-10;  
Matches 37; Conservative 2; Mismatches 10; Indels 10; Gaps 2;

QY 2 EKTPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAE-----AVRYADLLAKE 51  
|||||  
Db 9 ETTPPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAE-PEETPEKPEVDGYASTEATAAKE 66  
|||||

probable hemolysin YPO2045 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: A50249  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan  
I., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bar  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: A50249  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1576 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC90857.1; PID:g15980056; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO2045

Query Match 21.8%; Score 80.5; DB 2; Length 1576;  
Best Local Similarity 25.7%; Pred. No. 2.6;  
Matches 28; Conservative 13; Mismatches 25; Indels 43; Gaps 4;  
QY 1 KETPEEPKEEVIKANLIYADGKTQTAEFGK-----TFPE----- 36  
|||||  
Db 1001 KANTTEQKEGEVSLRG-----GMTATQETKGLGKVAETSGDGYAEMLVGNINAKSG 1054  
|||||  
QY 37 ----ATAEAYRYADLLAKENGYTAD-----LEDGGYTINIRFAG 72  
|||||  
Db 1055 VSIKTTGDVYYATNIEGGNGDITDAGNNLYFDVODSORSNNIKESG 1103  
|||||

## RESULT 6

T37931  
hypoetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T37931  
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.  
submitted to the EMBL Data Library, August 1999  
A:Reference number: 221755  
A:Accession: T37931  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-324 <MCD>  
A:Cross-references: EMBL:AL109820; PIDN:CAB52567.1; GSPDB:GN00066; SPDB:SPAC1952.0  
A:Experimental source: strain 972h-; cosmid C1952  
C:Genetics:  
A:Gene: SPDB:SPAC1952.03  
A:Map position: 1  
A:Introns: 144/3

Query Match 20.0%; Score 74; DB 2; Length 324;  
Best Local Similarity 30.2%; Pred. No. 2.2;  
Matches 19; Conservative 14; Mismatches 26; Indels 4; Gaps 1;  
QY 1 KETPEEPKEEVIKANLIYADGKTQTAEFGKTFEAATAEAYRYADLLAKENGYTADLE 60  
|||||  
Db 126 KENTPOPKKSRNRQKERL----ERRKAEMKMSQAELSEKMAADLKNEKKKFSKILE 181  
|||||  
QY 61 DGG 63  
:|  
Db 182 EAG 184  
:|

## RESULT 7

AD1525  
Probable cell surface protein (LPXTG motif) [imported] - Listeria innocua (strain C)  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AD1525  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blic  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fslf  
D.; Jones, L.M.; Karst, U.